

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/074,694
Source: IFW16
Date Processed by STIC: 07-05-2005

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/074,694

DATE: 07/05/2005

TIME: 14:27:54

Input Set : A:\10276-017002.TXT

Output Set: N:\CRF4\07052005\J074694.raw

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4 <110> APPLICANT: Kahn, C. Ronald
5   Zhu, Jianhua
7 <120> TITLE OF INVENTION: MODULATING THE RAD-NM23 INTERACTION
10 <130> FILE REFERENCE: 10276-017002
12 <140> CURRENT APPLICATION NUMBER: US 10/074,694
13 <141> CURRENT FILING DATE: 2002-02-12
15 <150> PRIOR APPLICATION NUMBER: US 09/053,967
16 <151> PRIOR FILING DATE: 1998-04-02
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 308
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 Met Thr Leu Asn Gly Gly Gly Ser Gly Ala Gly Gly Ser Arg Gly Gly
29 1          5          10          15
30 Gly Gln Glu Arg Glu Arg Arg Arg Gly Ser Thr Pro Trp Gly Pro Ala
31          20          25          30
32 Pro Pro Leu His Arg Arg Ser Met Pro Val Asp Glu Arg Asp Leu Gln
33          35          40          45
34 Ala Ala Leu Thr Pro Gly Ala Leu Thr Ala Ala Ala Ala Gly Thr Gly
35          50          55          60
36 Thr Gln Gly Pro Arg Leu Asp Trp Pro Glu Asp Ser Glu Asp Ser Leu
37 65          70          75          80
38 Ser Ser Gly Gly Ser Asp Ser Asp Glu Ser Val Tyr Lys Val Leu Leu
39          85          90          95
40 Leu Gly Ala Pro Gly Val Gly Lys Ser Ala Leu Ala Arg Ile Phe Gly
41          100         105         110
42 Gly Val Glu Asp Gly Pro Glu Ala Glu Ala Ala Gly His Thr Tyr Asp
43          115         120         125
44 Arg Ser Ile Val Val Asp Gly Glu Glu Ala Ser Leu Met Val Tyr Asp
45          130         135         140
46 Ile Trp Glu Gln Asp Gly Gly Arg Trp Leu Pro Gly His Cys Met Ala
47 145         150         155         160
48 Met Gly Asp Ala Tyr Val Ile Val Tyr Ser Val Thr Asp Lys Gly Ser
49          165         170         175
50 Phe Glu Lys Ala Ser Glu Leu Arg Val Gln Leu Arg Arg Ala Arg Gln
51          180         185         190
52 Thr Asp Asp Val Pro Ile Ile Leu Val Gly Asn Lys Ser Asp Leu Val
53          195         200         205
54 Arg Ser Arg Glu Val Ser Val Asp Glu Gly Arg Ala Cys Ala Val Val
55          210         215         220

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56 Phe Asp Cys Lys Phe Ile Glu Thr Ser Ala Ala Leu His His Asn Val
57 225                230                235                240
58 Gln Ala Leu Phe Glu Gly Val Val Arg Gln Ile Arg Leu Arg Arg Asp
59                245                250                255
60 Ser Lys Glu Ala Asn Ala Arg Arg Gln Ala Gly Thr Arg Arg Arg Glu
61                260                265                270
62 Ser Leu Gly Lys Lys Ala Lys Arg Phe Leu Gly Arg Ile Val Ala Arg
63                275                280                285
64 Asn Ser Arg Lys Met Ala Phe Arg Ala Lys Ser Lys Ser Cys His Asp
65                290                295                300
66 Leu Ser Val Leu
67 305
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 664
72 <212> TYPE: DNA
73 <213> ORGANISM: Mus musculus
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (1)...(498)
79 <400> SEQUENCE: 2
80 cag tcg cag ccg gcg gta aag cct tgt cat ctg aag ggg acc atg gcc 48
81 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
82 1 5 10 15
84 aac agt gag cgt acc ttc att gcc atc aag cct gat ggg gtc cag cgg 96
85 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
86 20 25 30
88 ggg ctg gtg ggc gag atc atc aag cgg ttc gag cag aag ggg ttc cgc 144
89 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
90 35 40 45
92 ctt gtt ggt ctg aag ttt ctg cag gct tca gag gac ctt ctc aag gag 192
93 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
94 50 55 60
96 cac tac act gac ctg aag gac cgc ccc ttc ttt act ggc ctg gtg aaa 240
97 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
98 65 70 75 80
100 tac atg cac tca gga cca gtg gtt gct atg gtc tgg gag ggt ctg aat 288
101 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
102 85 90 95
104 gtg gtg aag aca ggc cgc gtg atg ctt gga gag acc aac ccc gca gac 336
105 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
106 100 105 110
108 tct aag cct ggg acc ata cga gga gac ttc tgc att caa gtt ggc agg 384
109 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
110 115 120 125
112 aac atc att cat ggc agc gat tct gta aag agc gca gag aag gag atc 432
113 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
114 130 135 140
116 agc ttg tgg ttt cag cct gag gag ctg gtg gag tac aag agc tgt gcg 480
117 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala

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118 145          150          155          160
120 cag aac tgg atc tat gag tgataggacg gtgccggttt tctacctgct      528
121 Gln Asn Trp Ile Tyr Glu
122          165
124 tactcttggt ctcacaggca ggggaccagc aaccctagat atttctggaa cttctttgac 588
125 ctggaaggaa cctttgggag ccgtgactcc ctgtgcagtg ttacgtgccca ctgtagatt 648
126 aaagtgttta atctgt      664
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 166
130 <212> TYPE: PRT
131 <213> ORGANISM: Mus musculus
133 <400> SEQUENCE: 3
134 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
135 1          5          10          15
136 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
137          20          25          30
138 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
139          35          40          45
140 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
141          50          55          60
142 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
143 65          70          75          80
144 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
145          85          90          95
146 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
147          100          105          110
148 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
149          115          120          125
150 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
151          130          135          140
152 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
153 145          150          155          160
154 Gln Asn Trp Ile Tyr Glu
155          165
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 670
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <221> NAME/KEY: CDS
165 <222> LOCATION: (73)...(528)
167 <400> SEQUENCE: 4
168 cggccaacgag gcggaatccc ttctgtcttc ccagcgcagc gccgcgcgcc ggcccctcca 60
169 gcttcccggga cc atg gcc aac ctg gag cgc acc ttc atc gcc atc aag ccg 111
170          Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro
171          1          5          10
173 gac ggc gtg cag cgc ggc ctg gtg ggc gag atc atc aag cgc ttc gag      159
174 Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu
175          15          20          25

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177 cag aag gga ttc cgc ctc gtg gcc atg aag ttc ctc cgg gcc tct gaa 207
178 Gln Lys Gly Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu
179 30 35 40 45
181 gaa cac ctg aag cag cac tac att gac ctg aaa gac cga cca ttc ttc 255
182 Glu His Leu Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe
183 50 55 60
185 cct ggg ctg gtg aag tac atg aac tca ggg ccg gtt gtg gcc atg gtc 303
186 Pro Gly Leu Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val
187 65 70 75
189 tgg gag ggg ctg aac gtg gtg aag aca ggc cga gtg atg ctt ggg gag 351
190 Trp Glu Gly Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu
191 80 85 90
193 acc aat cca gca gat tca aag cca ggc acc att cgt ggg gac ttc tgc 399
194 Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys
195 95 100 105
197 att cag gtt ggc agg aac atc att cat ggc agt gat tca gta aaa agt 447
198 Ile Gln Val Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser
199 110 115 120 125
201 gct gaa aaa gaa atc agc cta tgg ttt aag cct gaa gaa ctg gtt gac 495
202 Ala Glu Lys Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp
203 130 135 140
205 tac aag tct tgt gct cat gac tgg gtc tat gaa taagaggtgg acacaacagc 548
206 Tyr Lys Ser Cys Ala His Asp Trp Val Tyr Glu
207 145 150
209 agtctccttc agcacggcgt ggtgtgtccc tggacacagc tcttcattcc attgacttag 608
210 aggcaacagg attgatcatt cttttataga gcatatttgc caataaagct tttggaagcc 668
211 gg 670
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 152
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 5
219 Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
220 1 5 10 15
221 Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly
222 20 25 30
223 Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu
224 35 40 45
225 Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu
226 50 55 60
227 Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
228 65 70 75 80
229 Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro
230 85 90 95
231 Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
232 100 105 110
233 Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys
234 115 120 125
235 Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser

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236	130	135	140
237	Cys Ala His Asp Trp Val Tyr Glu		
238	145	150	

VERIFICATION SUMMARY

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